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1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,328

DATE: 01/24/2002

TIME: 12:28

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01242002\I833328.raw

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 OFFICE OF PETITIONS

ENTERED

3 <110> APPLICANT: Laemmle, Bernhard
 4 Schwarz, Hans-Peter
 5 Scheifflinger, Friedrich
 6 Antoine, Gerhard
 7 Kerschbaumer, Randolph
 8 Tagliavacca, Luigina
 9 Zimmermann, Klaus
 10 Furlan, Miha
 11 Turecek, Peter
 12 Gerritsen, Helena E.
 14 <120> TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF)
 Protease Activity
 15 Comprising a Polypeptide Chain with the Amino Acid Sequence AAGGILHLELLV
 17 <130> FILE REFERENCE: 247.00CIP
 19 <140> CURRENT APPLICATION NUMBER: 09/833,328
 20 <141> CURRENT FILING DATE: 2001-04-12
 22 <150> PRIOR APPLICATION NUMBER: 09/721,254
 23 <151> PRIOR FILING DATE: 2000-11-22
 25 <160> NUMBER OF SEQ ID NOS: 15
 27 <170> SOFTWARE: PatentIn version 3.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 12
 31 <212> TYPE: PRT
 32 <213> ORGANISM: human
 34 <400> SEQUENCE: 1
 36 Ala Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val
 37 1 5 10
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 133
 42 <212> TYPE: PRT
 43 <213> ORGANISM: human
 45 <400> SEQUENCE: 2
 47 Pro Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val Leu
 48 1 5 10 15
 51 Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro Ser Leu Gly
 52 20 25 30
 55 Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr Glu Pro
 56 35 40 45
 59 Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser Leu Leu Ser
 60 50 55 60
 63 Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp Thr Asp Pro
 64 65 70 75 80
 67 Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp Leu Glu Leu
 68 85 90 95

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71 Pro Asp Gly Asn Arg Gln Val Arg Gly Val Thr Gln Leu Gly Gly Ala
72          100          105          110
75 Cys Ser Pro Thr Trp Ser Cys Leu Ile Thr Glu Asp Thr Gly Phe Asp
76          115          120          125
79 Leu Gly Val Thr Ile
80          130
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 444
85 <212> TYPE: DNA
86 <213> ORGANISM: human
88 <400> SEQUENCE: 3
89 gctgcaggcg gcatcctaca cctggagctg ctgggtggccg tgggccccga tgtcttcag      60
91 gctcaccagg aggacacaga gcgctatgtg ctaccaaac tcaacatcgg ggcagaactg      120
93 ctctcgggacc cgtccctggg ggctcagttt cgggtgcacc tgggtgaagat ggtcattctg      180
95 acagagcctg aggggtgcccc aaatatcaca gccaacctca cctcgtccct gctgagcgtc      240
97 tgtgggtgga gccagaccat caaccctgag gacgacacgg atcctggcca tgctgacctg      300
99 gtcctctata tactaggtt tgacctggag ttgcctgatg gtaaccggca ggtgcggggc      360
101 gtcaccagc tgggcggtgc ctgctcccca acctggagct gcctcattac cgaggacact      420
103 ggcttcgacc tgggagtcac catt                                444
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 148
108 <212> TYPE: PRT
109 <213> ORGANISM: human
111 <400> SEQUENCE: 4
113 Ala Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val Gly Pro
114 1          5          10          15
117 Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr
118          20          25          30
121 Asn Leu Asn Ile Gly Ala Glu Leu Arg Asp Pro Ser Leu Gly Ala
122          35          40          45
125 Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr Glu Pro Glu
126          50          55          60
129 Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser Leu Leu Ser Val
130 65          70          75          80
133 Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly
134          85          90          95
137 His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro
138          100          105          110
141 Asp Gly Asn Arg Gln Val Arg Gly Val Thr Gln Leu Gly Gly Ala Cys
142          115          120          125
145 Ser Pro Thr Trp Ser Cys Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu
146          130          135          140
149 Gly Val Thr Ile
150 145
153 <210> SEQ ID NO: 5
154 <211> LENGTH: 15
155 <212> TYPE: PRT
156 <213> ORGANISM: human
158 <400> SEQUENCE: 5

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161 1 5 10 15
164 <210> SEQ ID NO: 6
165 <211> LENGTH: 150
166 <212> TYPE: PRT
167 <213> ORGANISM: human
169 <400> SEQUENCE: 6
171 Arg Arg Ala Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val
172 1 5 10 15
175 Gly Pro Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val
176 20 25 30
179 Leu Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro Ser Leu
180 35 40 45
183 Gly Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr Glu
184 50 55 60
187 Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser Leu Leu
188 65 70 75 80
191 Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp Thr Asp
192 85 90 95
195 Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp Leu Glu
196 100 105 110
199 Leu Pro Asp Gly Asn Arg Gln Val Arg Gly Val Thr Gln Leu Gly Gly
200 115 120 125
203 Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile Thr Glu Asp Thr Gly Phe
204 130 135 140
207 Asp Leu Gly Val Thr Ile
208 145 150
211 <210> SEQ ID NO: 7
212 <211> LENGTH: 10
213 <212> TYPE: PRT
214 <213> ORGANISM: human
216 <400> SEQUENCE: 7
218 Ser Val Ser Gly Lys Pro Gln Tyr Met Val
219 1 5 10
222 <210> SEQ ID NO: 8
223 <211> LENGTH: 5
224 <212> TYPE: PRT
225 <213> ORGANISM: human
227 <400> SEQUENCE: 8
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230 1 5
233 <210> SEQ ID NO: 9
234 <211> LENGTH: 9
235 <212> TYPE: PRT
236 <213> ORGANISM: human
238 <400> SEQUENCE: 9
240 Ala Ala Gly Gly Ile Leu His Leu Glu
241 1 5
244 <210> SEQ ID NO: 10

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245 <211> LENGTH: 10
246 <212> TYPE: PRT
247 <213> ORGANISM: human
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252 1 5 10
255 <210> SEQ ID NO: 11
256 <211> LENGTH: 15
257 <212> TYPE: PRT
258 <213> ORGANISM: human
260 <400> SEQUENCE: 11
262 Ala Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val Gly
263 1 5 10 15
266 <210> SEQ ID NO: 12
267 <211> LENGTH: 5
268 <212> TYPE: PRT
269 <213> ORGANISM: human
271 <400> SEQUENCE: 12
273 Asn Gln Thr Val Ser
274 1 5
277 <210> SEQ ID NO: 13
278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: oligo primer
282 <400> SEQUENCE: 13
283 cggcgggatc ctacacctgg 20
286 <210> SEQ ID NO: 14
287 <211> LENGTH: 20
288 <212> TYPE: DNA
289 <213> ORGANISM: oligo primer
291 <400> SEQUENCE: 14
292 aatggtgact cccaggtcga 20
295 <210> SEQ ID NO: 15
296 <211> LENGTH: 136
297 <212> TYPE: PRT
298 <213> ORGANISM: human
300 <400> SEQUENCE: 15
302 Ala Val Gly Pro Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg
303 1 5 10 15
306 Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro
307 20 25 30
310 Ser Leu Gly Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu
311 35 40 45
314 Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser
315 50 55 60
318 Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp
319 65 70 75 80
322 Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp
323 85 90 95

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326	Leu	Glu	Leu	Pro	Asp	Gly	Asn	Arg	Gln	Val	Arg	Gly	Val	Thr	Gln	Leu
327				100					105					110		
330	Gly	Gly	Ala	Cys	Ser	Pro	Thr	Trp	Ser	Cys	Leu	Ile	Thr	Glu	Asp	Thr
331			115					120					125			
334	Gly	Phe	Asp	Leu	Gly	Val	Thr	Ile								
335		130						135								

VERIFICATION SUMMARY

DATE: 01/24/2002

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Input Set : A:\PTO.VSK.txt

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